

FIG. 1A

FIG. 1B

aaagaaggagccgacttcattctacttaactttcctttaaagataacttcccttgac 1500
ccaccattgtcagggttgtctccagtccctctggagggtatgttctggcggaggg 1560
gccatctgcatggaacttctcaccaaacagggtggagcagtgcctactccatagatca 1620
gtgatcatgcagatcagtgccacactggtaaggggaaagcacgagtcagttggagcc 1680
aacaatctcaatacagtctgacaagagcacagcagtcctacaagtcctggcagatc 1740
cacgaaaaaaaaacggctggtacacacaccccaaaagaagacggctaaccctggagtatcacc 1800
cttcctccctccccaggcaccactggaccaattaccttgaatgctgtattggatctca 1860
cgctgcctctgtggttccctccctcattttcctggacgtgatagctctgcctattgcag 1920
gacaatgatggctattctaaacgctaaggaaaaaaaaacaaacacagaactgttcaagta 1980
ctcaagactgacttacagaccaaccaaccaccccttgctggacccttgctcaggcattc 2040
ttataaaagaaaacttcgagcctccttatattgctggaaactcagctgtgctccagacta 2100
gagcctccttacctatgctatggatttttaatttatttctttatcatgtacactgc 2160
ttttttggttacagtgtatgtatggatgtatgaaaaaaaaatgtatcttggaaaacaa 2220
ttacagttgttaattgaaaaaaaaaaaaaaaaa 2280

(SEQ ID NO:1)

FIG. 2A

CTCGCTCCTCTCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGC
GCTGACCCCTTCGCGGGGGGATGCGTCATTATCAGATCAAGACCAACCGGTCA
CCCTCTCCGGCCCCGGCGGGGGCGGGCGCCGGCGCTTGGTACTCTAGATAACCTC
GGGCCGATCGCACGCCCGTGGCGGACGACCCATTGCAACGTCTGCCCTATCAACT
TTCGATGGTAGTCGCCGTGCTACCATGGTACCGACGGGTACGGGGATCAGGGTTCGA
TTCCGGAGAGGGAGGCGCTGAGAAACGGCTACCACATCCAAGGAAGGACAGCAGGCGCGCAA
TTACCCACTCCCAGGGTGGCGGCCATCTGGCAAGGGGGATCAGGAAGTGC
GACCGCGGCGGCGGCCGGCGGGCGGGCGGGAGCCGGAGCGCAGGCCGAGGGCTC
CCGGCCCGCCGGCCCCGGAGCGGAGCGGAGGATGCAAGCAGCCGAGCCGAGGGG
M Q Q P Q P Q G
CAGCAGCAGCCGGGGCCGGGGCAGCAGCTGGGGGGCAGGGGGCGGCCGGGGGGGG
Q Q Q P G P G Q Q L G G Q G A A P G A G
GGCGGCCAGGGGGGGCCGGGGCCGGGGCCCTGCCCTGAGGCGAGAGCTGAAGCTGCTC
G G P G G G P G P C L R R E L K L L
GAGTCCATCTCCACCGCGGCCACGAGCGCTTCCGCATTGCCAGCGCCTGCCCTGACGAG
E S I F H R G H E R F R I A S A C L D E
CTGAGCTGCGAGTCCCTGCTGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
L S C E F L L A G A G G A G A G A A P G
CCGCATCTCCCCCACGGGGTCGGTGCCTGGGATCCTGCGCATCCACTGCAACATC
P H L P P R G S V P G D P V R I H C N I
ACGGAGTCATACCTCTGCTGCCCCCATCTGGTCGGTGGAGTCTGATGACCTAACTTG
T E S Y P A V P P I W S V E S D D P N L
GCTGCTGTCTGGAGAGGCTGGACATAAAAGAAAGGAATACTCTGCTATTGCAGCAT
A A V L E R L V D I K K G N T L L L Q H
CTGAAGAGGATCATCTCGACCTGTGTAACCTATAACCTCCCTCAGCATCCAGATGTG
L K R I I S D L C K L Y N L P Q H P D V
GAGATGCTGGATCAACCCCTGCCAGCAGAGCAGTCACACAGGAAGACGTGCTTCAGAA
E M L D Q P L P A E Q C T Q E D V S S E
GATGAAGATGAGGAGATGCCCTGAGGACACAGAACACTTAGATCACTATGAAATGAAAGAG
D E D E E M P E D T E D L D H Y E M K E
GAAGAGCCAGCTGAGGGCAAGAAATCTGAAGATGATGGCATTGGAAAAGAAAATTGGCC
E E P A E G K K S E D D G I G K E N L A
ATCCTAGAGAAAATTAAAAAGAACCAAGAGGCAAGATTACTTAAATGGTCAGTGTCTGGC
I L E K I K K N Q R Q D Y L N G A V S G
TCGGTGCAGGCCACTGACCGGCTGATGAAGGAGCTCAGGGATATACCGATCACAGAGT
S V Q A T D R L M K E L R D I Y R S Q S
TTCAAAGGCGGAAACTATGCACTGCAACTCGTGAATGACAGTCTGTATGATTGGAAATGTC
F K G G N Y A V E L V N D S L Y D W N V
AAACTCCTCAAAGTTGACCAGGACAGCGCTTGCACAACGATCTCCAGATCCTCAAAGAG
K L L K V D Q D S A L H N D L Q I L K E
AAAGAAGGAGCCGACTTCATTCACTTAACTTTCTTAAAGATAACTTCCCTTGAC
K E G A D F I L L N F S F K D N F P F D
CCACCATTGTCAGGGTTGTCTCCAGTCCTCTGGAGGGTATGTTCTGGGGGGAGGG
P P F V R V V S P V L S G G Y V L G G G
GCCATCTGCATGGAACCTCTCACCAACAGGGCTGGAGCAGTCCTACTCCATAGAGTCA
A I C M E L L T K Q G W S S A Y S I E S
GTGATCATGCAGATCAGTGCCACACTGGTGAAGGGAAAGCACGAGTCAGTTGGAGCC
V I M Q I S A T L V K G K A R V Q F G A

FIG. 2B

AACAAATCTCAATACAGTCTGACAAGAGCACAGCAGTCCTACAAGTCCTGGTGCAGATC
N K S Q Y S L T R A Q Q S Y K S L V Q I
CACGAAAAAAACGGCTGGTACACACCCCCAAAGAAGACGGCTAACCTGGAGTATCACC
H E K N G W Y T P P K E D G *
CTTCCTCCCTCCCCAGGCACCACTGGACCAATTACCTTGAATGCTGTATTTGGATCTCA
CGCTGCCTCTGTGGTCCCTCCCTCATTTTCCTGGACGTGATAGCTCTGCCTATTGCAG
GACAATGATGGCTATTCTAACGCTAACGGAAAAAAACAAACACAGAACTGTTCAAGTA
CTCAAGACTGACTTACAGACCAACCAACCACCTGCTGGAACCCCTGCTAGCAGGCATTC
TTATAAAAGAAACTTCGAGCCTCCTTATATTGCTGGAAACTCAGCTGTGCTCCAGACTA
GAGCCTCCTTACCTATGCTATGGATTTAATTATTTCTCTTATTCATGTACACTGC
TTTTTTGGTTACAGTGTATGGATGTGTATGAAAAAAATGTATCTTGGGAAAACAA
TTACAGTTGTTAATTGAAAAAAACAA

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FIG. 3

MQQPQPQGQQ	QPGPGQQLGG	QGAAPGAGGG	PGGGPGPGPC	40
LRRELKLLES	IFHRGHERFR	IASACLDELS	CEFLLAGAGG	80
AGAGAAPGPH	LPPRGSVPGD	PVRIHCNITE	SYPAVPPIWS	120
VESDDPNLAA	VLERLVDIKK	GNTLLLQHLK	RIISDLCKLY	160
NLPQHPDVEM	LDQPLPAEQC	TQEDVSSEDE	DEEMPEDTED	200
LDHYEMKEEE	PAEGKKSEDD	GIGKENLAIL	EKIKKNQRQD	240
YLNGAVSGSV	QATDRLMKEL	RDIYRSQSFK	GGNYAVELVN	280
DSLYDWNVKL	LKVDQDSALH	NDLQILKEKE	GADFILLNFS	320
FKDNFPFDPP	FVRVVSPVLS	GGYVLGGGAI	CMELLTKQGW	360
SSAYSIESVI	MQISATLVKG	KARVQFGANK	SQYSLTRAQQ	400
SYKSLVQIHE	KNGWYTPPKE	DG		422

(SEQ ID NO:2)

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FIG. 4

1 65

RATL1d6 (1) MQQPQPQQPQPGQQQLGGQGAAPGAGGGPGGGPGPGPCIRRELKLESIFHRGHERFRIASAC
T21349_F25H2.8_Cel (1) -----MACLRKIKEDIQVLEKLFPKNHNRFQQLSAS
AAF45767_EG:25E8_Dr (1) -----MACLNTIKQEIKTLEKIFPKNHERFQJLNSS

66 130

RATL1d6 (66) LDELSCEFLLAGAGGAGAGAAPGPHLPPRGSVPGDPVRIHCNITESYPAVPPIWSVESDDPNLAA
T21349_F25H2.8_Cel (32) VDELSMKFINAEN-----KG-----IIVTANIQENYPRQPPIWFSSESDDVPVIG
AAF45767_EG:25E8_Dr (32) VDELLCRFIDKNG-----KR-----YDIHANITEYPPSPPVWFAESEETSVTN

131 195

RATL1d6 (131) VLERLVDIKKGNTLLLQHLKRIISDLCKLYNLPQHPDVEMLDQPL-----
T21349_F25H2.8_Cel (76) MSLQRLTETEESTNLHQHRLVSDLCSFYNLQMPCELPQIAPPVRDD-----IDEGRGSDI
AAF45767_EG:25E8_Dr (76) AVQILSNTNGRDNHVINQVGILLRELCKRLHNVPPLPPDIDNLALPLQTTPPSASPLRCEQRPGGGG

196 260

RATL1d6 (176) -----PAEQCTQEDVSSEDEDEEMPEDTEDLDHYEMKEEPAEGKKSEDDGIGKENIAILEKIK
T21349_F25H2.8_Cel (133) SDTTSEPIDDDMAGDGEVDDDDEEEEDDEDADGDEIEVEMAEDPTSQHDVGVSKEGLDMDKVS
AAF45767_EG:25E8_Dr (141) AGGGGGPHGNEETSDQEEIEDPIGESEQESEGDEDLPLEMDVRSTSKKDDMEVEHLATLEKLR
P52483_UB6B_MOUSE (1) -----MSSDRQRSDDESPSTSSGSSDADQRDP

261 325

RATL1d6 (235) KNQRQDYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVELVN-DSLYDWNVKLLKVDQDSA
T21349_F25H2.8_Cel (198) KINRQHLDGKVQGSITATDRLMKEIRDIHRSEHFKNGIYTFELEKEENLYQWWIKLHKVDEDSP
AAF45767_EG:25E8_Dr (206) QSQRQDYLKGGSVSGSVQATDRLMKELRDIYRSDAFKKNMYSIELVN-ESIYEWNIRLKSVPDSP
P52483_UB6B_MOUSE (28) AAPKPEEQERKPSATQQKNTKLSKTTAKLSTSAKRIQELAEITLDPPPNCASAGPKGCDNIYE
P27924_UBC1_HUMAN (1) -----MANIAVORIJKREFKEVLKSEETSKNQIKVDLVD-----ENFT-E
CAA72184_UBCD4_Dr (1) -----MANMAVSRRIKREFKEVMRSEEIVQCSIKIELVN-----DSWTE
P14682_UBC3_YEAST (1) -----MSSRKSTASSLLRQYRELTDPPKAIPSFHIELEDD-----SNIFTW

326 390

RATL1d6 (299) LHNDLQILKEKEGA-DFILLNFSFKDNFPFDPPFVRVVSPVLSGGYVLLGGAICMELLTKQG-----
T21349_F25H2.8_Cel (263) LFEDMKKLKKDHQ-DHILFSFTFNEKFPDCPPFVRVVAPHINQGFVLLGGAICMELLTKQG-----
AAF45767_EG:25E8_Dr (270) LHSDLQMLKEKEGK-DSILLNIFLKETYPFEPFPFVRVVHPITISGGYVLLGGAICMELLTKQG-----
P52483_UB6B_MOUSE (93) WRSTILGPPGSVYEGGVFELDITFSSDYPFKPPKVITRTRTRVHVNINSQ-GVICLCLDILKD-----
P27924_UBC1_HUMAN (39) LRGEIAGPPDTPYEGGRYOLEIJKIPETYPFNPKVRFITKIHWPNISSVTGAICLCLDILKD-----
CAA72184_UBCD4_Dr (39) LRGEIAGPPDTPYEGGKVELEIKVPETYPFNPKVRFITRIVHWPNISSVTGAICLCLDILKD-----
P14682_UBC3_YEAST (43) NIGVMVLNEDSIYHGGFPKAQMRFPEDFPFSPPQFRFTPAIYHPNVYRD-GRLCISILHQSGDP

391 455

RATL1d6 (360) -----WSSAYSIESVIMQISATLVKGKARVQFGANK-----SQYSLTRAQQSYKSLVQI
T21349_F25H2.8_Cel (324) -----WSSAYSIESCILQIAATLVKGARISFDAKHT-----STYSMARAQQSEFKSLOQI
AAF45767_EG:25E8_Dr (331) -----WSSAYTVEAVIMQIAATLVKGKARIQFGATKALTQ-----GQYSLARAQQSFKSLVQI
P52483_UB6B_MOUSE (153) -----WSPALTISKVLLSICSLLTDCNPADPLVGSIAT-----QYLTNRAEHDRARIQWT
P27924_UBC1_HUMAN (100) -----WAAAMTILRTVLLSLOQALAAAEPDDPQDAVVAN-----QYKQNPEMFQQTARLWA
CAA72184_UBCD4_Dr (100) -----WAAAMTILRTVLLSLOQALAAAEPDDPQDAVVAY-----QFKDKYDLFLLTAKHWT
P14682_UBC3_YEAST (107) TDEPDAETWSPVQITVESVLISIVSLLEDPNINSPANVDAAVDYRKNPQEYKQRVKMEVERSQDI

456 520

RATL1d6 (409) HEKNGWYTPPKEDG-----
T21349_F25H2.8_Cel (374) HANSGCTFLCSTPSSHFFAHLVFFLHSDDFFFNGFLKSETFTFFKLSFRGYISSLVLYSFSRHL
AAF45767_EG:25E8_Dr (384) HEKNGWTPPKEDG-----
P52483_UB6B_MOUSE (203) KRYAT-----
P27924_UBC1_HUMAN (150) HVYAGAPVSSPEYTKKIENLCAMGFDRNAIVALSSKSWDVETATELLLSN-----
CAA72184_UBCD4_Dr (150) NAYAGGPHTFPDCCDSKIQRLRDMGIDEHEARAVLSKENWNIEKATEGLFS-----
P14682_UBC3_YEAST (172) PKGFIMPTESEAYISQSKLDEPESNKDMADNFWYDSDLDDENGSVILQDDDYDDGNNHIPFEDD

521 579

T21349_F25H2.8_Cel (439) HHPFFTRFLIPQLQPPPPIPQLIPPFLNRTKHV-----
P14682_UBC3_YEAST (237) DVVNYNDNDDDERIEFEDDDDDDSIDNDSVMDRKQPHKAEDESEDVEDVERVSKKI

FIG. 5A

RATL1d6 BLAST results/alignment w/ *Drosophila* protein

FIG. 5B

RATL1d6 BLAST results/alignment w/ *C. elegans* protein

>GCGPROT:Q93571 F25H2.8 PROTEIN.
Length = 471
Score = 317 bits (805), Expect = 6e-86
Identities = 178/397 (44%), Positives = 247/397 (61%), Gaps = 49/397 (12%)

Query: 41 LRRELKLLESIFHRGHERFRIASACLDELSCEFLLAGAGGAAPGPHLPPRGSVPGD 100
L+ +++LE +F + H RF+I SA +DELS +F+ A G
Sbjct: 7 LKEDIQVLEKLFPKNHNRFQILSASVDELSMKFINAENKG----- 46

Query: 101 PVRIHCNITESYPAVPPIWSVESDD-PNLAAVLERLVDIKKGNTLLLQHLKRIISDLCKL 159
+ + NI E+YP PPIW ESDD P + L+RL + ++ +T +L + R++SDLC
Sbjct: 47 -IIVTANIQENYPRQPPWFSESDDPVIGMSLQRLTETEE-STNILHQVHRLVSDLCSF 104

Query: 160 YNL-----PQHPDVE-----MLDQPLPAEQCTQEDVSSEDEDEEMPEDTE 199
YNL P D++ +P+ + +V +DE+EE ED +
Sbjct: 105 YNLQMPCELPQIAPPVRDDIDEGRGSDISDTTSEPIDDDMAGDGEVDDDDEEEEDDEDAD 164

Query: 200 -DLDHYEMKEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLNGAVSGSVQATDRLMK 258
D++ EM EE+P D G+ KE L +L+K+ K RQ +L+G V GS+ ATDRLMK
Sbjct: 165 GDIEIVEMAEDPTS---QHDVGVSKEGLDMLDKVSKINRQQHLDGKVQGSITATDRLMK 221

Query: 259 ELRDIYRSQSFKGNYAVELVND-SLYDWNVKLLKVDQDSALHNDLQILKEKEGADFILL 317
E+RDI+RS+ FK G Y EL + +LY W +KL KVD+DS L D++ LK+ D +L
Sbjct: 222 EIRDIHRSEHFKNGIYTFELEKEENLYQWWIKLHKVDEDSPFEDMKKLKKDHNQDHLLF 281

Query: 318 NFSFKDNFPFDPPFVRRVSPVLSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATL 377
+F+F + FP DPPFVRRV+P ++ G+VLGGGAICMELLTKQGWSSAYSIES I+QI+ATL
Sbjct: 282 SFTFNEKFPDCPPFVRRVAPHINQGFVLGGGAICMELLTKQGWSSAYSIESCILQIAATL 341

Query: 378 VKGKARVQFGA-NKSQYSLTRAQQSYKSLVQIHEKNG 413
VKG+AR+ F A + S YS+ RAQQS+KSL QIH K+G
Sbjct: 342 VKGRARISFDAKHTSTYSMARAQQSFKSLQQIHKSG 378

FIG. 6

